

Requirement, Applicant will therefore petition the Commission to request that the Restriction Requirement be withdrawn with respect to Groups I-III and that all claims be examined together.

Objection to the specification

The Examiner objected to the specification as containing "an embedded hyperlink and/or other form of browser executable code." The specification has been amended to delete this material. Applicants therefore request that the objection be withdrawn.

The specification was also objected to for referencing two patent applications, and an updated status was requested. At this time, the patent applications are still pending and the status remains the same.

Objection to the claims

Claims 1-4 and 6-8 were rejected as allegedly failing to provide proper antecedent basis for the claimed subject matter, for allegedly failing to disclose a detailed description or working example of a method for identifying a compound that modulates sensory signaling in cells comprising contacting the compound with a G-protein alpha subunit polypeptide and measuring binding of radiolabeled GTP to the polypeptide. Applicants respectfully traverse. Support is provided in the specification, e.g., at page 4, lines 19-25, page 5, lines 7-9, and in the claims as originally filed. Furthermore, claim 1 has been amended to clarify the phrase "sensory signaling" refers to sensory signal transduction. Support for this amendment can be found, e.g., in the specification at page 3, line 23 and page 7, lines 23-28. Applicants respectfully request that the rejection be withdrawn.

Rejection under 35 U.S.C. § 112, second paragraph

Sensory signaling

Claims 1-4 and 6-8 were rejected as allegedly indefinite for reciting the phrase "sensory signaling." Applicants respectfully traverse. However, to expedite prosecution, the

claims have been amended to delete the phrase "sensory signaling" and recite the phrase "signal transduction." Support for this amendment can be found, e.g., in the specification at page 3, line 23 and page 7, lines 23-28. Applicants respectfully request that the rejection be withdrawn.

"Modulation of sensory signaling"

The Examiner states that claims 1-4 and 6-8 "recite identifying a compound that modulates sensory signaling in sensory cells" but that the methods steps do not achieve the goal stated in the preamble. Claim 1 has been amended to refer to the preamble. Applicants therefore respectfully request that the rejection be withdrawn.

"Binding"

Claims 1-4 and 6-8 were rejected as allegedly indefinite because the claims do not recite what type of binding will occur, e.g., an increase, a decrease, or no change in binding. Applicants respectfully traverse. The specification on page 13, lines 6-17 describe that determining the function effect refers to an assay that "increases or decreases" a parameter that is directly or indirectly under the influence of the claimed G-protein alpha subunit. As the specification clearly describes the type of binding that will occur, e.g., an increase or a decrease, Applicants respectfully request that the rejection be withdrawn.

"GTP"

Claim 6 was rejected as allegedly indefinite for reciting the acronym "GTP." Applicants respectfully traverse. This term is accepted as a term of art by those of ordinary skill in the art and as such meets the clarity and precision standards of the statute. Applicants respectfully request that the rejection be withdrawn.

Rejection under 35 U.S.C. §103

Claims 1-4 and 6-8 were rejected as allegedly unpatentable over Freissmuth in view of Wilkie. Freissmuth teaches a general method for identifying compounds that modulate G proteins. Wilkie teaches amino acid sequence of SEQ ID NO:2. Applicants respectfully traverse.

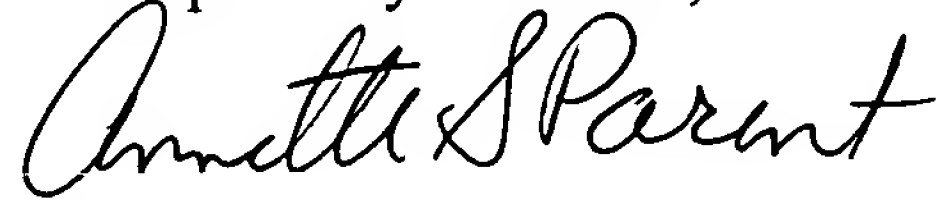
As explained below, the Examiner has not established a prima facie case of obviousness. In order to establish a prima facie case of obviousness, the Examiner must demonstrate: (1) that the cited references teach or disclose all the claim elements; (2) that the prior art suggests that one of skill in the art modify or combine the reference teachings; and (3) that there is a reasonable expectation of success by one of skill in the art. MPEP § 2143.

The cited references fail to teach or disclose all the claim elements. The present claims are directed to a method of identifying modulators of signal transduction in sensory cells. None of the cited references disclose that the claimed G protein alpha subunit is expressed in a sensory cell, specifically, a taste receptor cell. Applicants therefore respectfully request that the rejection be withdrawn.

CONCLUSION

If the Examiner has any questions regarding Applicant's response, or if the Examiner believes that a telephone conference would expedite consideration of this matter in any way, please call the undersigned at 415-576-0200.

Respectfully submitted,



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APPENDIX A

SPECIFICATION: VERSION WITH MARKINGS TO SHOW CHANGES MADE

Please amend the paragraph on page 20, line 10 to page 21, lines 4, as follows by deleting the material at page 20, line 17 as indicated. The full paragraph is provided.

A preferred example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990), respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information [(http://www.ncbi.nlm.nih.gov/)]. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength

(W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

APPENDIX B

CLAIMS: VERSION WITH MARKINGS TO SHOW CHANGES MADE

1. (once amended) A method for identifying a compound that modulates [sensory signaling] signal transduction in sensory cells, the method comprising the steps of:
 - (i) contacting the compound with a sensory cell specific G-protein alpha subunit polypeptide, the G-protein alpha subunit polypeptide comprising greater than 70% amino acid sequence identity to a polypeptide having a sequence of SEQ ID NO:2; and
 - (ii) determining a functional effect of the compound upon the G-protein alpha subunit polypeptide, thereby identifying a compound that modulates signal transduction in sensory cells.